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REVIEWSStory contributed by Alison Mitchell, [Nature Reviews Molecular Cell Biology](#)

The *Drosophila* protein EAST is involved in the assembly of a nucleoskeleton that may prevent chromosome collisions.

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The beginning of the END

What do traditional office skills like filing and book-keeping have in common with cell biology? The answer lies in the organization of essential components - be they documents or proteins - into distinct compartments. Take the nucleus, for example, where the proteins involved in processes such as transcription and RNA metabolism are physically clustered, and chromosomes are partitioned into discrete territories.

Reporting in [Nature Cell Biology](#), Martin Wasser and William Chia from the National University of Singapore describe a molecular secretary that may organize this nuclear filing system in the fruit fly *Drosophila melanogaster*. Known as EAST (for 'enhanced adult sensory threshold'), it contains 12 potential proteolytic sites as well as seven putative nuclear-localization signals. These characteristics led the authors to propose that EAST is an unstable protein targeted specifically to the nucleus.

To test this prediction, Wasser and Chia studied the expression pattern of EAST in giant nuclei from *Drosophila* salivary glands. Confocal microscopy captured images of EAST in a region that the authors refer to as the extrachromosomal nuclear domain (END), which, as its name suggests, is the area around and between the chromosomes. Similar compartments have previously been detected in other organisms, where they are thought to belong to a putative nuclear endoskeleton.

What might be the function of EAST within this 'nucleoskeleton'? The authors reasoned that, if it is involved in forming a structural backbone, EAST may recruit other factors to the END. So they studied the effect of disrupting the east gene on distribution of a protein called CP60 that normally co-localizes with EAST. Consistent with their ideas, the CP60 expression pattern was destroyed. What's more, Wasser and Chia found overlapping expression patterns between EAST and nuclear actin - a satisfying discovery given that, outside the nucleus, actin is a core structural component of the cytoskeleton.

Overexpression of EAST gave equally striking results - an expansion of the END. This effect, which can also be induced by heat-shocking *Drosophila*, results from accumulation of the extra EAST. But as the figure shows, the consequences of expansion vary depending where the END expands: if EAST accumulates mainly between the chromosomes (left), the effect will be to increase the spacing between them; expansion between the chromosomes and nuclear membrane (right), however, will compress the chromosomes. In either case, this could prevent the random collision of neighbouring chromosome arms when cells are under stress.

Wasser and Chia have shown, then, that EAST is a nuclear architect involved in the assembly of an expandable nucleoskeleton between chromosomes. The next steps will be to work out how increased levels of EAST cause the END to expand, and to take a closer look at how the EAST protein is regulated.

Live PubMed searches

[|| The nucleoskeleton ||](#) [REVIEWS on the nuclear matrix ||](#)

Genome tutorial

[|| Find CP60 in the *Drosophila* genome ||](#)

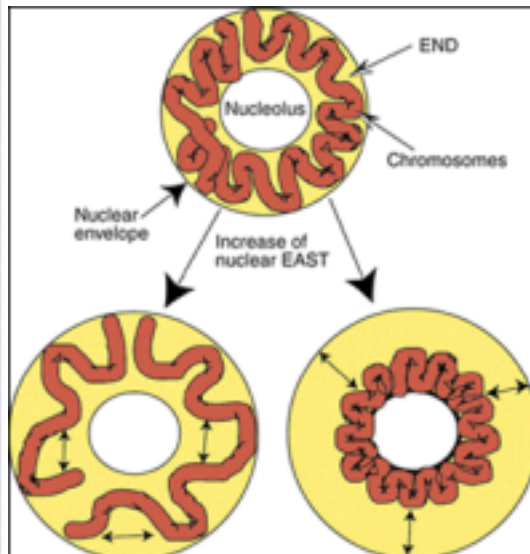
Further NCBI resources

[|| CP60 in LocusLink ||](#)
[|| *Drosophila* homepage ||](#)

Comments? Questions?

We would welcome feedback on NCBI's Coffee Break.

Email to: info@ncbi.nlm.nih.gov

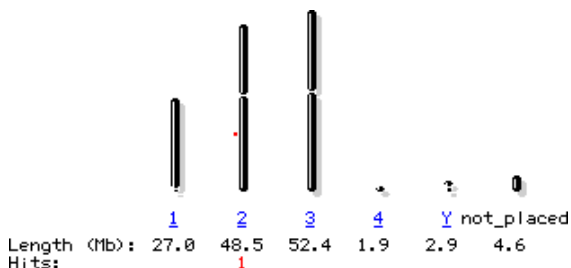


The EAST protein from *Drosophila* may be involved in the assembly of a **nucleoskeleton**. When overexpressed, EAST expands the extrachromosomal nuclear domain (END) - the space between chromosomes. The consequences of expansion vary depending where the END expands: if EAST accumulates mainly between the chromosomes (left), the effect will be to increase the spacing between them; expansion between the chromosomes and nuclear membrane (right), however, will compress the chromosomes. In either case, this could prevent the random collision of neighbouring chromosome arms when cells are under stress.

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Search for
[on chromosome\(s\)](#)

Drosophila melanogaster genome view



Precomputed BLAST results:
Enter any protein ID (accession or gi number) to find matches to *Drosophila* genome proteins

Protein ID

Search results for query "CP60": 1 hit

All data displayed on these pages are based on the sequence provided by Celera and the Berkeley Drosophila Genome Project. Searching this sequence for CP60 shows one hit, localized on chromosome 2, in the dynamically drawn figure (above).

The table below lists the hits, and the corresponding sequence information, if any. In this case, the Celera/Berkeley genome has been annotated to include CP60, so the sequence view (sv), genbank view (gv), etc, of this segment is available.

Click on the Map60 link in the Map Element column to view the MAP60 gene within its genomic context.

Chr	Match	Map element
2	Cp60	Map60 sv gb gr fr gp fp b ll fb gf

Links:

Map element - *Map view*

Nucleotide:

- [sv](#) Sequence Viewer
- [gb](#) GenBank view of record
- [gr](#) GenBank view of region
- [fr](#) FASTA format of region

Protein:

- [gp](#) GenPept view
- [fp](#) FASTA protein format

Resources:

- [b](#) Precomputed BLAST
- [ll](#) LocusLink
- [fb](#) FlyBase
- [gf](#) GadFly

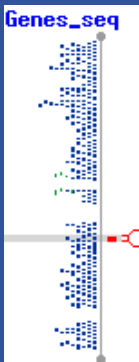
Search for

On chromosome(s)

Find

HELP
FTP

Region
Shown: 31,211K
32,181K
Go



Drosophila melanogaster Map View

There are 137 genes in this genomic region, of which 20 (including CP60) are displayed. To alter the map display, [click on Display Settings](#).

Zoom controls, plus the location of this section of the chromosome, are found in the left margin. A pop-up box that displays a choice of a zoom or sequence-viewing functions can be triggered by clicking either on the map itself or on the chromosome locator.

Chromosome: [1](#) [2](#) [3](#) [4](#) [Y](#)

Query: Map60 [\[clear\]](#)

Master: Gene Sequence Map

[Display settings](#)

Total Genes On Map: 5055

Region Displayed: 31,211K-32,181Kbp

Genes Listed: 20 Total Genes in Region: 137

	Symbol	CytoPosition	Size	Links
Genes_seq	CG8078	-	1154	sv gb gr fr gp fp b ll fb gf
	CG8781	-	586	sv gb gr fr gp fp b ll fb gf
	CG8057	-	2368	sv gb gr fr gp fp b ll fb gf
	CG8014	-	8981	sv gb gr fr gp fp b ll fb gf
	hig	45C-45C	19448	sv gb gr fr gp fp b ll fb gf
	TXBP181-like	-	2589	sv gb gr fr gp fp b ll fb gf
	CG11803	-	262	sv gb gr fr gp fp b ll fb gf
	CG13955	-	1204	sv gb gr fr gp fp b ll fb gf
	CG12933	-	1660	sv gb gr fr gp fp b ll fb gf
	CG1874	-	2972	sv gb gr fr gp fp b ll fb gf
	Map60	46A-46A	1898	sv gb gr fr gp fp b ll fb gf
	CG12927	-	632	sv gb gr fr gp fp b ll fb gf
	CG1773	-	1164	sv gb gr fr gp fp b ll fb gf
	CG1648	-	8556	sv gb gr fr gp fp b ll fb gf
	CG1665	-	1258	sv gb gr fr gp fp b ll fb gf
	CG1675	-	830	sv gb gr fr gp fp b ll fb gf
	CG1441	-	4259	sv gb gr fr gp fp b ll fb gf
	CG12133	-	1204	sv gb gr fr gp fp b ll fb gf
	CG12129	-	1407	sv gb gr fr gp fp b ll fb gf
	CG12921	-	374	sv gb gr fr gp fp b ll fb gf

Search for

[On chromosome\(s\)](#)

Find

Genomic Biology

FTP site

About this sequence
release

Sequencing Centers

Celera

BDGP

Related Resources

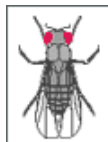
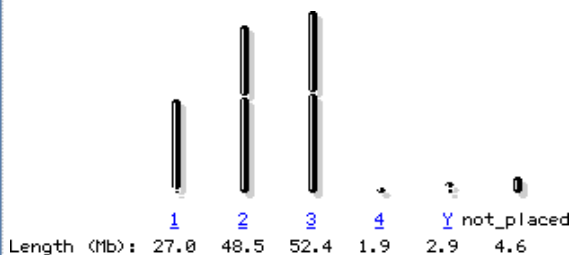
FlyBase

GadFly

The Interactive Fly

Drosophila melanogaster genome

Genome Overview



The assembled and annotated genome sequence of the euchromatic arms of the five *Drosophila melanogaster* (fruit fly) chromosomes is now available in GenBank. The sequence, determined in a collaboration between [Celera](#) and the [Berkeley Drosophila Genome Project](#), is described in the March 24, 2000 issue of [Science](#). The ~137 Mb of sequence, most of which is found on chromosomes 1 (also known as X), 2, and 3, contains ~13,500 annotated genes. ~2470 of these genes correlate with a known gene described in [FlyBase](#). FlyBase provides sequence for an additional ~500 genes that are not annotated on the Celera/BDGP sequence.

From early observations of the banding patterns of its polytene chromosomes to current work on mRNA and protein gradients in the developing embryo, *Drosophila melanogaster* has been studied in biology labs for over eighty years. Many of the genes that define the spatial pattern of cell types and body parts have now been identified, along with the regulatory pathways in which they operate. As a number of these genes have counterparts in higher eukaryotes, the study of the *Drosophila* developmental program provides insight into human development as well. *Drosophila* is the second multicellular organism to be sequenced, after the nematode [Caenorhabditis elegans](#).

Resources

▶ Get sequence data by [FTP](#)

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[Map View](#)
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▶ Search for genes in [LocusLink](#)

▶ [Related Structures:](#)
Drosophila genome proteins with sequence similarity to proteins with known structure

▶ [BLAST](#) your sequence against the *Drosophila melanogaster* genome

▶ Precomputed BLAST results: [\[More...\]](#)

Enter the gene or protein ID of a *Drosophila* genome sequence protein to view protein matches in all organisms

Drosophila Gene or

Protein ID

Show

Enter the ID (accession or gi number) of a protein from any organism to view matches to *Drosophila* genome sequence proteins

Any Protein ID

Show

Questions or Comments?
Write to the [NCBI Service Desk](#)

Revised May 9, 2000